

On page 35, please replace the first full paragraph with the following text:

Q2
As indicated above, there is little if any sequence homology shared among the amino termini of $G\alpha$ subunits. The amino terminal domains of $G\alpha$ subunits that precede the first β -sheet (containing the sequence motif -LLLLGAGESG- (SEQ ID NO: 2); see Noel et al., *Supra*, for the numbering of the structural elements of $G\alpha$ subunits) vary in length from 41 amino acids (GPA1) to 31 amino acids ($G\alpha t$). Most $G\alpha$ subunits share the consensus sequence for the addition of myristic acid at their amino termini (MGxxxS-), although not all $G\alpha$ subunits that contain this motif have myristic acid covalently associated with the glycine at position 2 (Speigel et al., TIES 16: 338-3441, 1991). The role of this post-translational modification has been inferred from studies in which the activity of mutant $G\alpha$ subunits from which the consensus sequence for myristoylation has been added or deleted has been assayed (Mumby et al., Proc. Natl. Acad. Sci. USA 87: 728-732 1990; Linder et al., J. Biol. Chem. 266: 4654-4659, 1991; Gallego et al., Proc. Natl. Acad. Sci. USA 89: 9695-9699, 1992). These studies suggest two roles for N-terminal myristoylation. First, the presence of amino-terminal myristic acid has in some cases been shown to be required for association of $G\alpha$ subunits with the membrane, and second, this modification has been demonstrated to play a role in modulating the association of $G\alpha$ subunits with $G\beta\gamma$ complexes. The role of myristoylation of the GPA1 gene products is, at present, unknown.

The replacement paragraph presented above incorporates changes as indicated by the marked-up version below.

Some aspects of $G\alpha$ structure are relevant to the design of modified $G\alpha$ subunits. The amino terminal 66 residues of GPA1 are aligned with the cognate domains of human $G\alpha s$, $G\alpha i2$, $G\alpha i3$, $G\alpha i6$ and transducin. In the GPA1 $G\alpha$ hybrids, the amino terminal 41 residues (derived from GPA1) are identical, end with the sequence-LEKQRDKNE- (SEQ ID NO: 1) and are underlined for emphasis. All residues following the glutamate (E) residue at position 41 are contributed by the human $G\alpha$ subunits, including the consensus nucleotide binding motif -GxGxxG-. Periods in the sequences indicate gaps that have been introduced to maximize alignments in this region. Codon bias is mammalian. For alignments of the entire coding regions of GPA1 with $G\alpha s$, $G\alpha i$, and $G\alpha o$, $G\alpha q$ and $G\alpha z$, see Dietzel and Kurjan (Cell 50: 573, 1987) and Lambright et al. (Nature 369: 621-628, 1994). Additional sequence information is provided by Mattera et al. (FEBS Lett 206: 36-41, 1986), Bray et al. (Proc. Natl. Acad. Sci. USA 83: 8893-8897, 1986) and Bray et al. (Proc. Natl. Acad. Sci. USA 84: 5115-5119, 1987).

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